

SEQUENCE LISTING



<110> SHONE, Clifford Charles  
SUTTON, John Mark  
HALLIS, Bassam  
SILMAN, Nigel

<120> Delivery of Superoxide Dismutase to Neuronal Cells

<130> 1581.0800000

<140> 09/831,050

<141> 1999-11-05

<150> PCT/GB99/03699

<151> 1998-11-05

<160> 14

<170> PatentIn Ver. 2.1

<210> 1

<211> 204

<212> PRT

<213> Bacillus caldotenax

<400> 1

Met Pro Phe Glu Leu Pro Ala Leu Pro Tyr Pro Tyr Asp Ala Leu Glu  
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Pro His Ile Asp Lys Glu Thr Met Asn Ile His His Thr Lys His His  
20 25 30

Asn Thr Tyr Val Thr Asn Leu Asn Ala Ala Leu Glu Gly His Pro Asp  
35 40 45

Leu Gln Asn Lys Ser Leu Glu Glu Leu Leu Ser Asn Leu Glu Ala Leu  
50 55 60

Pro Glu Ser Ile Arg Thr Ala Val Arg Asn Asn Gly Gly Gly His Ala  
65 70 75 80

Asn His Ser Leu Phe Trp Thr Ile Leu Ser Pro Asn Gly Gly Gly Glu  
85 90 95

Pro Thr Gly Glu Leu Ala Glu Ala Ile Asn Lys Lys Phe Gly Ser Phe  
100 105 110

Thr Ala Phe Lys Asp Glu Phe Ser Lys Ala Ala Ala Gly Arg Phe Gly  
115 120 125

Ser Gly Trp Ala Trp Leu Val Val Asn Asn Gly Glu Leu Glu Ile Thr  
130 135 140

Ser Thr Pro Asn Gln Asp Ser Pro Ile Met Glu Gly Lys Thr Pro Ile  
145 150 155 160

Leu Gly Leu Asp Val Trp Glu His Ala Tyr Tyr Leu Lys Tyr Gln Asn  
165 170 175

Arg Arg Pro Glu Tyr Ile Ala Ala Phe Trp Asn Ile Val Asn Trp Asp  
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Glu Val Ala Lys Arg Tyr Ser Glu Ala Lys Ala Lys  
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<210> 2  
<211> 204  
<212> PRT  
<213> Bacillus stearothermophilus

<400> 2  
Met Pro Phe Glu Leu Pro Ala Leu Pro Tyr Pro Tyr Asp Ala Leu Glu  
1 5 10 15  
Pro His Ile Asp Lys Glu Thr Met Asn Ile His His Thr Lys His His  
20 25 30  
Asn Thr Tyr Val Thr Asn Leu Asn Ala Ala Leu Glu Gly His Pro Asp  
35 40 45  
Leu Gln Asn Lys Ser Leu Glu Glu Leu Leu Ser Asn Leu Glu Ala Leu  
50 55 60  
Pro Glu Ser Ile Arg Thr Ala Val Arg Asn Asn Gly Gly Gly His Ala  
65 70 75 80  
Asn His Ser Leu Phe Trp Thr Ile Leu Ser Pro Asn Gly Gly Gly Glu  
85 90 95  
Pro Thr Gly Glu Leu Ala Asp Ala Ile Asn Lys Lys Phe Gly Ser Phe  
100 105 110  
Thr Ala Phe Lys Asp Glu Phe Ser Lys Ala Ala Ala Gly Arg Phe Gly  
115 120 125  
Ser Gly Trp Ala Trp Leu Val Val Asn Asn Gly Glu Leu Glu Ile Thr  
130 135 140  
Ser Thr Pro Asn Gln Asp Ser Pro Ile Met Glu Gly Lys Thr Pro Ile  
145 150 155 160  
Leu Gly Leu Asp Val Trp Glu His Ala Tyr Tyr Leu Lys Tyr Gln Asn  
165 170 175  
Arg Arg Pro Glu Tyr Ile Ala Ala Phe Trp Asn Val Val Asn Trp Asp  
180 185 190  
Glu Val Ala Lys Arg Tyr Ser Glu Ala Lys Ala Lys  
195 200

<210> 3  
<211> 1067  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:construct

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Met Pro Phe Glu Leu Pro Ala Leu Pro Tyr Pro Tyr Asp Ala Leu Glu  
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Pro His Ile Asp Lys Glu Thr Met Asn Ile His His Thr Lys His His  
20 25 30  
Asn Thr Tyr Val Thr Asn Leu Asn Ala Ala Leu Glu Gly His Pro Asp  
35 40 45

Leu	Gln	Asn	Lys	Ser	Leu	Glu	Glu	Leu	Leu	Ser	Asn	Leu	Glu	Ala	Leu
50						55					60				
Pro	Glu	Ser	Ile	Arg	Thr	Ala	Val	Arg	Asn	Asn	Gly	Gly	Gly	His	Ala
65					70				75						80
Asn	His	Ser	Leu	Phe	Trp	Thr	Ile	Leu	Ser	Pro	Asn	Gly	Gly	Gly	Glu
				85					90					95	
Pro	Thr	Gly	Glu	Leu	Ala	Asp	Ala	Ile	Asn	Lys	Lys	Phe	Gly	Ser	Phe
			100					105					110		
Thr	Ala	Phe	Lys	Asp	Glu	Phe	Ser	Lys	Ala	Ala	Ala	Gly	Arg	Phe	Gly
		115					120					125			
Ser	Gly	Trp	Ala	Trp	Leu	Val	Val	Asn	Asn	Gly	Glu	Leu	Glu	Ile	Thr
	130					135					140				
Ser	Thr	Pro	Asn	Gln	Asp	Ser	Pro	Ile	Met	Glu	Gly	Lys	Thr	Pro	Ile
145					150					155					160
Leu	Gly	Leu	Asp	Val	Trp	Glu	His	Ala	Tyr	Tyr	Leu	Lys	Tyr	Gln	Asn
				165					170					175	
Arg	Arg	Pro	Glu	Tyr	Ile	Ala	Ala	Phe	Trp	Asn	Val	Val	Asn	Trp	Asp
			180					185						190	
Glu	Val	Ala	Lys	Arg	Tyr	Ser	Glu	Ala	Lys	Ala	Lys	Gln	Arg	Ser	Cys
		195					200					205			
Gly	Leu	Val	Pro	Arg	Gly	Ser	Gly	Pro	Gly	Ser	Ala	Leu	Asn	Asp	Leu
	210					215					220				
Cys	Ile	Lys	Val	Asn	Asn	Trp	Asp	Leu	Phe	Phe	Ser	Pro	Ser	Glu	Asp
225					230					235					240
Asn	Phe	Thr	Asn	Asp	Leu	Asn	Lys	Gly	Glu	Glu	Ile	Thr	Ser	Asp	Thr
				245					250					255	
Asn	Ile	Glu	Ala	Ala	Glu	Glu	Asn	Ile	Ser	Leu	Asp	Leu	Ile	Gln	Gln
			260					265					270		
Tyr	Tyr	Leu	Thr	Phe	Asn	Phe	Asp	Asn	Glu	Pro	Glu	Asn	Ile	Ser	Ile
		275					280					285			
Glu	Asn	Leu	Ser	Ser	Asp	Ile	Ile	Gly	Gln	Leu	Glu	Leu	Met	Pro	Asn
	290					295					300				
Ile	Glu	Arg	Phe	Pro	Asn	Gly	Lys	Lys	Tyr	Glu	Leu	Asp	Lys	Tyr	Thr
305					310					315					320
Met	Phe	His	Tyr	Leu	Arg	Ala	Gln	Glu	Phe	Glu	His	Gly	Lys	Ser	Arg
				325					330					335	
Ile	Ala	Leu	Thr	Asn	Ser	Val	Asn	Glu	Ala	Leu	Leu	Asn	Pro	Ser	Arg
			340					345					350		
Val	Tyr	Thr	Phe	Phe	Ser	Ser	Asp	Tyr	Val	Lys	Lys	Val	Asn	Lys	Ala
		355					360					365			
Thr	Glu	Ala	Ala	Met	Phe	Leu	Gly	Trp	Val	Glu	Gln	Leu	Val	Tyr	Asp
	370					375					380				
Phe	Thr	Asp	Glu	Thr	Ser	Glu	Val	Ser	Thr	Thr	Asp	Lys	Ile	Ala	Asp
385					390					395					400

Ile	Thr	Ile	Ile	Ile	Pro	Tyr	Ile	Gly	Pro	Ala	Leu	Asn	Ile	Gly	Asn	
				405					410					415		
Met	Leu	Tyr	Lys	Asp	Asp	Phe	Val	Gly	Ala	Leu	Ile	Phe	Ser	Gly	Ala	
			420					425					430			
Val	Ile	Leu	Leu	Glu	Phe	Ile	Pro	Glu	Ile	Ala	Ile	Pro	Val	Leu	Gly	
		435					440					445				
Thr	Phe	Ala	Leu	Val	Ser	Tyr	Ile	Ala	Asn	Lys	Val	Leu	Thr	Val	Gln	
	450					455					460					
Thr	Ile	Asp	Asn	Ala	Leu	Ser	Lys	Arg	Asn	Glu	Lys	Trp	Asp	Glu	Val	
465					470					475					480	
Tyr	Lys	Tyr	Ile	Val	Thr	Asn	Trp	Leu	Ala	Lys	Val	Asn	Thr	Gln	Ile	
				485					490					495		
Asp	Leu	Ile	Arg	Lys	Lys	Met	Lys	Glu	Ala	Leu	Glu	Asn	Gln	Ala	Glu	
			500					505					510			
Ala	Thr	Lys	Ala	Ile	Ile	Asn	Tyr	Gln	Tyr	Asn	Gln	Tyr	Thr	Glu	Glu	
		515				520					525					
Glu	Lys	Asn	Asn	Ile	Asn	Phe	Asn	Ile	Asp	Asp	Leu	Ser	Ser	Lys	Leu	
	530					535					540					
Asn	Glu	Ser	Ile	Asn	Lys	Ala	Met	Ile	Asn	Ile	Asn	Lys	Phe	Leu	Asn	
545					550					555					560	
Gln	Cys	Ser	Val	Ser	Tyr	Leu	Met	Asn	Ser	Met	Ile	Pro	Tyr	Gly	Val	
				565					570					575		
Lys	Arg	Leu	Glu	Asp	Phe	Asp	Ala	Ser	Leu	Lys	Asp	Ala	Leu	Leu	Lys	
			580				585						590			
Tyr	Ile	Tyr	Asp	Asn	Arg	Gly	Thr	Leu	Ile	Gly	Gln	Val	Asp	Arg	Leu	
	595					600						605				
Lys	Asp	Lys	Val	Asn	Asn	Thr	Leu	Ser	Thr	Asp	Ile	Pro	Phe	Gln	Leu	
	610					615					620					
Ser	Lys	Tyr	Val	Asp	Asn	Gln	Arg	Leu	Leu	Ser	Thr	Phe	Thr	Glu	Tyr	
625					630					635					640	
Ile	Lys	Asn	Ile	Ile	Asn	Thr	Ser	Ile	Leu	Asn	Leu	Arg	Tyr	Glu	Ser	
				645					650					655		
Asn	His	Leu	Ile	Asp	Leu	Ser	Arg	Tyr	Ala	Ser	Lys	Ile	Asn	Ile	Gly	
		660						665					670			
Ser	Lys	Val	Asn	Phe	Asp	Pro	Ile	Asp	Lys	Asn	Gln	Ile	Gln	Leu	Phe	
		675					680					685				
Asn	Leu	Glu	Ser	Ser	Lys	Ile	Glu	Val	Ile	Leu	Lys	Asn	Ala	Ile	Val	
	690					695					700					
Tyr	Asn	Ser	Met	Tyr	Glu	Asn	Phe	Ser	Thr	Ser	Phe	Trp	Ile	Arg	Ile	
705					710					715					720	
Pro	Lys	Tyr	Phe	Asn	Ser	Ile	Ser	Leu	Asn	Asn	Glu	Tyr	Thr	Ile	Ile	
				725					730					735		
Asn	Cys	Met	Glu	Asn	Asn	Ser	Gly	Trp	Lys	Val	Ser	Leu	Asn	Tyr	Gly	
			740					745					750			

Glu	Ile	Ile	Trp	Thr	Leu	Gln	Asp	Thr	Gln	Glu	Ile	Lys	Gln	Arg	Val	
		755					760					765				
Val	Phe	Lys	Tyr	Ser	Gln	Met	Ile	Asn	Ile	Ser	Asp	Tyr	Ile	Asn	Arg	
	770					775					780					
Trp	Ile	Phe	Val	Thr	Ile	Thr	Asn	Asn	Arg	Leu	Asn	Asn	Ser	Lys	Ile	
785					790					795					800	
Tyr	Ile	Asn	Gly	Arg	Leu	Ile	Asp	Gln	Lys	Pro	Ile	Ser	Asn	Leu	Gly	
				805					810					815		
Asn	Ile	His	Ala	Ser	Asn	Asn	Ile	Met	Phe	Lys	Leu	Asp	Gly	Cys	Arg	
			820					825					830			
Asp	Thr	His	Arg	Tyr	Ile	Trp	Ile	Lys	Tyr	Phe	Asn	Leu	Phe	Asp	Lys	
		835					840					845				
Glu	Leu	Asn	Glu	Lys	Glu	Ile	Lys	Asp	Leu	Tyr	Asp	Asn	Gln	Ser	Asn	
	850					855					860					
Ser	Gly	Ile	Leu	Lys	Asp	Phe	Trp	Gly	Asp	Tyr	Leu	Gln	Tyr	Asp	Lys	
865					870					875					880	
Pro	Tyr	Tyr	Met	Leu	Asn	Leu	Tyr	Asp	Pro	Asn	Lys	Tyr	Val	Asp	Val	
				885					890					895		
Asn	Asn	Val	Gly	Ile	Arg	Gly	Tyr	Met	Tyr	Leu	Lys	Gly	Pro	Arg	Gly	
			900					905					910			
Ser	Val	Met	Thr	Thr	Asn	Ile	Tyr	Leu	Asn	Ser	Ser	Leu	Tyr	Arg	Gly	
		915					920					925				
Thr	Lys	Phe	Ile	Ile	Lys	Lys	Tyr	Ala	Ser	Gly	Asn	Lys	Asp	Asn	Ile	
	930					935					940					
Val	Arg	Asn	Asn	Asp	Arg	Val	Tyr	Ile	Asn	Val	Val	Val	Lys	Asn	Lys	
945					950					955					960	
Glu	Tyr	Arg	Leu	Ala	Thr	Asn	Ala	Ser	Gln	Ala	Gly	Val	Glu	Lys	Ile	
				965					970					975		
Leu	Ser	Ala	Leu	Glu	Ile	Pro	Asp	Val	Gly	Asn	Leu	Ser	Gln	Val	Val	
			980					985					990			
Val	Met	Lys	Ser	Lys	Asn	Asp	Gln	Gly	Ile	Thr	Asn	Lys	Cys	Lys	Met	
		995				1000						1005				
Asn	Leu	Gln	Asp	Asn	Asn	Gly	Asn	Asp	Ile	Gly	Phe	Ile	Gly	Phe	His	
	1010					1015					1020					
Gln	Phe	Asn	Asn	Ile	Ala	Lys	Leu	Val	Ala	Ser	Asn	Trp	Tyr	Asn	Arg	
1025					1030					1035					1040	
Gln	Ile	Glu	Arg	Ser	Ser	Arg	Thr	Leu	Gly	Cys	Ser	Trp	Glu	Phe	Ile	
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<210> 4

<211> 1070

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:construct

<400> 4

Met	Pro	Phe	Glu	Leu	Pro	Ala	Leu	Pro	Tyr	Pro	Tyr	Asp	Ala	Leu	Glu
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Pro	His	Ile	Asp	Lys	Glu	Thr	Met	Asn	Ile	His	His	Thr	Lys	His	His
			20					25					30		
Asn	Thr	Tyr	Val	Thr	Asn	Leu	Asn	Ala	Ala	Leu	Glu	Gly	His	Pro	Asp
		35					40					45			
Leu	Gln	Asn	Lys	Ser	Leu	Glu	Glu	Leu	Leu	Ser	Asn	Leu	Glu	Ala	Leu
	50					55					60				
Pro	Glu	Ser	Ile	Arg	Thr	Ala	Val	Arg	Asn	Asn	Gly	Gly	Gly	His	Ala
65					70					75					80
Asn	His	Ser	Leu	Phe	Trp	Thr	Ile	Leu	Ser	Pro	Asn	Gly	Gly	Gly	Glu
				85					90						95
Pro	Thr	Gly	Glu	Leu	Ala	Asp	Ala	Ile	Asn	Lys	Lys	Phe	Gly	Ser	Phe
			100					105					110		
Thr	Ala	Phe	Lys	Asp	Glu	Phe	Ser	Lys	Ala	Ala	Ala	Gly	Arg	Phe	Gly
		115					120					125			
Ser	Gly	Trp	Ala	Trp	Leu	Val	Val	Asn	Asn	Gly	Glu	Leu	Glu	Ile	Thr
	130					135					140				
Ser	Thr	Pro	Asn	Gln	Asp	Ser	Pro	Ile	Met	Glu	Gly	Lys	Thr	Pro	Ile
145					150					155					160
Leu	Gly	Leu	Asp	Val	Trp	Glu	His	Ala	Tyr	Tyr	Leu	Lys	Tyr	Gln	Asn
				165					170					175	
Arg	Arg	Pro	Glu	Tyr	Ile	Ala	Ala	Phe	Trp	Asn	Val	Val	Asn	Trp	Asp
			180					185					190		
Glu	Val	Ala	Lys	Arg	Tyr	Ser	Glu	Ala	Lys	Ala	Lys	Gln	Arg	Ser	Cys
		195					200					205			
Gly	Leu	Val	Pro	Arg	Gly	Ser	Gly	Pro	Gly	Ser	Lys	Ala	Pro	Gly	Ile
	210					215					220				
Cys	Ile	Asp	Val	Asp	Asn	Glu	Asp	Leu	Phe	Phe	Ile	Ala	Asp	Lys	Asn
225					230					235					240
Ser	Phe	Ser	Asp	Asp	Leu	Ser	Lys	Asn	Glu	Arg	Ile	Glu	Tyr	Asn	Thr
				245					250					255	
Gln	Ser	Asn	Tyr	Ile	Glu	Asn	Asp	Phe	Pro	Ile	Asn	Glu	Leu	Ile	Leu
			260					265					270		
Asp	Thr	Asp	Leu	Ile	Ser	Lys	Ile	Glu	Leu	Pro	Ser	Glu	Asn	Thr	Glu
		275					280					285			
Ser	Leu	Thr	Asp	Phe	Asn	Val	Asp	Val	Pro	Val	Tyr	Glu	Lys	Gln	Pro
	290					295					300				
Ala	Ile	Lys	Lys	Ile	Phe	Thr	Asp	Glu	Asn	Thr	Ile	Phe	Gln	Tyr	Leu
305					310					315					320
Tyr	Ser	Gln	Thr	Phe	Pro	Leu	Asp	Ile	Arg	Asp	Ile	Ser	Leu	Thr	Ser
				325					330					335	

Ser	Phe	Asp	Asp	Ala	Leu	Leu	Phe	Ser	Asn	Lys	Val	Tyr	Ser	Phe	Phe	340	345	350	
Ser	Met	Asp	Tyr	Ile	Lys	Thr	Ala	Asn	Lys	Val	Val	Glu	Ala	Gly	Leu	355	360	365	
Phe	Ala	Gly	Trp	Val	Lys	Gln	Ile	Val	Asn	Asp	Phe	Val	Ile	Glu	Ala	370	375	380	
Asn	Lys	Ser	Asn	Thr	Met	Asp	Lys	Ile	Ala	Asp	Ile	Ser	Leu	Ile	Val	385	390	395	400
Pro	Tyr	Ile	Gly	Leu	Ala	Leu	Asn	Val	Gly	Asn	Glu	Thr	Ala	Lys	Gly	405	410	415	
Asn	Phe	Glu	Asn	Ala	Phe	Glu	Ile	Ala	Gly	Ala	Ser	Ile	Leu	Leu	Glu	420	425	430	
Phe	Ile	Pro	Glu	Leu	Leu	Ile	Pro	Val	Val	Gly	Ala	Phe	Leu	Leu	Glu	435	440	445	
Ser	Tyr	Ile	Asp	Asn	Lys	Asn	Lys	Ile	Ile	Lys	Thr	Ile	Asp	Asn	Ala	450	455	460	
Leu	Thr	Lys	Arg	Asn	Glu	Lys	Trp	Ser	Asp	Met	Tyr	Gly	Leu	Ile	Val	465	470	475	480
Ala	Gln	Trp	Leu	Ser	Thr	Val	Asn	Thr	Gln	Phe	Tyr	Thr	Ile	Lys	Glu	485	490	495	
Gly	Met	Tyr	Lys	Ala	Leu	Asn	Tyr	Gln	Ala	Gln	Ala	Leu	Glu	Glu	Ile	500	505	510	
Ile	Lys	Tyr	Arg	Tyr	Asn	Ile	Tyr	Ser	Glu	Lys	Glu	Lys	Ser	Asn	Ile	515	520	525	
Asn	Ile	Asp	Phe	Asn	Asp	Ile	Asn	Ser	Lys	Leu	Asn	Glu	Gly	Ile	Asn	530	535	540	
Gln	Ala	Ile	Asp	Asn	Ile	Asn	Asn	Phe	Ile	Asn	Gly	Cys	Ser	Val	Ser	545	550	555	560
Tyr	Leu	Met	Lys	Lys	Met	Ile	Pro	Leu	Ala	Val	Glu	Lys	Leu	Leu	Asp	565	570	575	
Phe	Asp	Asn	Thr	Leu	Lys	Lys	Asn	Leu	Leu	Asn	Tyr	Ile	Asp	Glu	Asn	580	585	590	
Lys	Leu	Tyr	Leu	Ile	Gly	Ser	Ala	Glu	Tyr	Glu	Lys	Ser	Lys	Val	Asn	595	600	605	
Lys	Tyr	Leu	Lys	Thr	Ile	Met	Pro	Phe	Asp	Leu	Ser	Ile	Tyr	Thr	Asn	610	615	620	
Asp	Thr	Ile	Leu	Ile	Glu	Met	Phe	Asn	Lys	Tyr	Asn	Ser	Glu	Ile	Leu	625	630	635	640
Asn	Asn	Ile	Ile	Leu	Asn	Leu	Arg	Tyr	Lys	Asp	Asn	Asn	Leu	Ile	Asp	645	650	655	
Leu	Ser	Gly	Tyr	Gly	Ala	Lys	Val	Glu	Val	Tyr	Asp	Gly	Val	Glu	Leu	660	665	670	
Asn	Asp	Lys	Asn	Gln	Phe	Lys	Leu	Thr	Ser	Ser	Ala	Asn	Ser	Lys	Ile	675	680	685	

Arg	Val	Thr	Gln	Asn	Gln	Asn	Ile	Ile	Phe	Asn	Ser	Val	Phe	Leu	Asp	690	695	700
Phe	Ser	Val	Ser	Phe	Trp	Ile	Arg	Ile	Pro	Lys	Tyr	Lys	Asn	Asp	Gly	705	710	715
Ile	Gln	Asn	Tyr	Ile	His	Asn	Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Lys	725	730	735
Asn	Asn	Ser	Gly	Trp	Lys	Ile	Ser	Ile	Arg	Gly	Asn	Arg	Ile	Ile	Trp	740	745	750
Thr	Leu	Ile	Asp	Ile	Asn	Gly	Lys	Thr	Lys	Ser	Val	Phe	Phe	Glu	Tyr	755	760	765
Asn	Ile	Arg	Glu	Asp	Ile	Ser	Glu	Tyr	Ile	Asn	Arg	Trp	Phe	Phe	Val	770	775	780
Thr	Ile	Thr	Asn	Asn	Leu	Asn	Asn	Ala	Lys	Ile	Tyr	Ile	Asn	Gly	Lys	785	790	795
Leu	Glu	Ser	Asn	Thr	Asp	Ile	Lys	Asp	Ile	Arg	Glu	Val	Ile	Ala	Asn	805	810	815
Gly	Glu	Ile	Ile	Phe	Lys	Leu	Asp	Gly	Asp	Ile	Asp	Arg	Thr	Gln	Phe	820	825	830
Ile	Trp	Met	Lys	Tyr	Phe	Ser	Ile	Phe	Asn	Thr	Glu	Leu	Ser	Gln	Ser	835	840	845
Asn	Ile	Glu	Glu	Arg	Tyr	Lys	Ile	Gln	Ser	Tyr	Ser	Glu	Tyr	Leu	Lys	850	855	860
Asp	Phe	Trp	Gly	Asn	Pro	Leu	Met	Tyr	Asn	Lys	Glu	Tyr	Tyr	Met	Phe	865	870	875
Asn	Ala	Gly	Asn	Lys	Asn	Ser	Tyr	Ile	Lys	Leu	Lys	Lys	Asp	Ser	Pro	885	890	895
Val	Gly	Glu	Ile	Leu	Thr	Arg	Ser	Lys	Tyr	Asn	Gln	Asn	Ser	Lys	Tyr	900	905	910
Ile	Asn	Tyr	Arg	Asp	Leu	Tyr	Ile	Gly	Glu	Lys	Phe	Ile	Ile	Arg	Arg	915	920	925
Lys	Ser	Asn	Ser	Gln	Ser	Ile	Asn	Asp	Asp	Ile	Val	Arg	Lys	Glu	Asp	930	935	940
Tyr	Ile	Tyr	Leu	Asp	Phe	Phe	Asn	Leu	Asn	Gln	Glu	Trp	Arg	Val	Tyr	945	950	955
Thr	Tyr	Lys	Tyr	Phe	Lys	Lys	Glu	Glu	Glu	Lys	Leu	Phe	Leu	Ala	Pro	965	970	975
Ile	Ser	Asp	Ser	Asp	Glu	Phe	Tyr	Asn	Thr	Ile	Gln	Ile	Lys	Glu	Tyr	980	985	990
Asp	Glu	Gln	Pro	Thr	Tyr	Ser	Cys	Gln	Leu	Leu	Phe	Lys	Lys	Asp	Glu	995	1000	1005
Glu	Ser	Thr	Asp	Glu	Ile	Gly	Leu	Ile	Gly	Ile	His	Arg	Phe	Tyr	Glu	1010	1015	1020
Ser	Gly	Ile	Val	Phe	Glu	Glu	Tyr	Lys	Asp	Tyr	Phe	Cys	Ile	Ser	Lys	1025	1030	1035
																		1040



Trp Tyr Leu Lys Glu Val Lys Arg Lys Pro Tyr Asn Leu Lys Leu Gly  
1045 1050 1055

Cys Asn Trp Gln Phe Ile Pro Lys Asp Glu Gly Trp Thr Glu  
1060 1065 1070

<210> 5

<211> 1059

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:construct

<400> 5

Met Pro Phe Glu Leu Pro Ala Leu Pro Tyr Pro Tyr Asp Ala Leu Glu  
1 5 10 15

Pro His Ile Asp Lys Glu Thr Met Asn Ile His His Thr Lys His His  
20 25 30

Asn Thr Tyr Val Thr Asn Leu Asn Ala Ala Leu Glu Gly His Pro Asp  
35 40 45

Leu Gln Asn Lys Ser Leu Glu Glu Leu Leu Ser Asn Leu Glu Ala Leu  
50 55 60

Pro Glu Ser Ile Arg Thr Ala Val Arg Asn Asn Gly Gly Gly His Ala  
65 70 75 80

Asn His Ser Leu Phe Trp Thr Ile Leu Ser Pro Asn Gly Gly Gly Glu  
85 90 95

Pro Thr Gly Glu Leu Ala Asp Ala Ile Asn Lys Lys Phe Gly Ser Phe  
100 105 110

Thr Ala Phe Lys Asp Glu Phe Ser Lys Ala Ala Ala Gly Arg Phe Gly  
115 120 125

Ser Gly Trp Ala Trp Leu Val Val Asn Asn Gly Glu Leu Glu Ile Thr  
130 135 140

Ser Thr Pro Asn Gln Asp Ser Pro Ile Met Glu Gly Lys Thr Pro Ile  
145 150 155 160

Leu Gly Leu Asp Val Trp Glu His Ala Tyr Tyr Leu Lys Tyr Gln Asn  
165 170 175

Arg Arg Pro Glu Tyr Ile Ala Ala Phe Trp Asn Val Val Asn Trp Asp  
180 185 190

Glu Val Ala Lys Arg Tyr Ser Glu Ala Lys Ala Lys Gln Arg Ser Cys  
195 200 205

Gly Leu Val Pro Arg Gly Ser Gly Pro Gly Ser Lys Ala Pro Pro Arg  
210 215 220

Leu Cys Ile Arg Val Asn Asn Arg Glu Leu Phe Phe Val Ala Ser Glu  
225 230 235 240

Ser Ser Tyr Asn Glu Asn Asp Ile Asn Thr Pro Lys Glu Ile Asp Asp  
245 250 255

Thr Thr Asn Leu Asn Asn Asn Tyr Arg Asn Asn Leu Asp Glu Val Ile

260					265					270					
Leu	Asp	Tyr	Asn	Ser	Glu	Thr	Ile	Pro	Gln	Ile	Ser	Asn	Gln	Thr	Leu
	275						280					285			
Asn	Thr	Leu	Val	Gln	Asp	Asp	Ser	Tyr	Val	Pro	Arg	Tyr	Asp	Ser	Asn
	290					295					300				
Gly	Thr	Ser	Glu	Ile	Glu	Glu	His	Asn	Val	Val	Asp	Leu	Asn	Val	Phe
	305					310					315				320
Phe	Tyr	Leu	His	Ala	Gln	Lys	Val	Pro	Glu	Gly	Glu	Thr	Asn	Ile	Ser
				325					330					335	
Leu	Thr	Ser	Ser	Ile	Asp	Thr	Ala	Leu	Ser	Glu	Glu	Ser	Gln	Val	Tyr
			340					345					350		
Thr	Phe	Phe	Ser	Ser	Glu	Phe	Ile	Asn	Thr	Ile	Asn	Lys	Pro	Val	His
		355					360					365			
Ala	Ala	Leu	Phe	Ile	Ser	Trp	Ile	Asn	Gln	Val	Ile	Arg	Asp	Phe	Thr
	370					375					380				
Thr	Glu	Ala	Thr	Gln	Lys	Ser	Thr	Phe	Asp	Lys	Ile	Ala	Asp	Ile	Ser
	385					390					395				400
Leu	Val	Val	Pro	Tyr	Val	Gly	Leu	Ala	Leu	Asn	Ile	Gly	Asn	Glu	Val
			405						410					415	
Gln	Lys	Glu	Asn	Phe	Lys	Glu	Ala	Phe	Glu	Leu	Leu	Gly	Ala	Gly	Ile
			420					425					430		
Leu	Leu	Glu	Phe	Val	Pro	Glu	Leu	Leu	Ile	Pro	Thr	Ile	Leu	Val	Phe
		435					440					445			
Thr	Ile	Lys	Ser	Phe	Ile	Gly	Ser	Ser	Glu	Asn	Lys	Asn	Lys	Ile	Ile
	450					455					460				
Lys	Ala	Ile	Asn	Asn	Ser	Leu	Met	Glu	Arg	Glu	Thr	Lys	Trp	Lys	Glu
	465					470					475				480
Ile	Tyr	Ser	Trp	Ile	Val	Ser	Asn	Trp	Leu	Thr	Arg	Ile	Asn	Thr	Gln
			485						490					495	
Phe	Asn	Lys	Arg	Lys	Glu	Gln	Met	Tyr	Gln	Ala	Leu	Gln	Asn	Gln	Val
			500					505					510		
Asp	Ala	Ile	Lys	Thr	Val	Ile	Glu	Tyr	Lys	Tyr	Asn	Asn	Tyr	Thr	Ser
		515					520					525			
Asp	Glu	Arg	Asn	Arg	Leu	Glu	Ser	Glu	Tyr	Asn	Ile	Asn	Asn	Ile	Arg
	530					535					540				
Glu	Glu	Leu	Asn	Lys	Lys	Val	Ser	Leu	Ala	Met	Glu	Asn	Ile	Glu	Arg
	545					550					555				560
Phe	Ile	Thr	Glu	Ser	Ser	Ile	Phe	Tyr	Leu	Met	Lys	Leu	Ile	Asn	Glu
			565						570					575	
Ala	Lys	Val	Ser	Lys	Leu	Arg	Glu	Tyr	Asp	Glu	Gly	Val	Lys	Glu	Tyr
			580					585					590		
Leu	Leu	Asp	Tyr	Ile	Ser	Glu	His	Arg	Ser	Ile	Leu	Gly	Asn	Ser	Val
		595					600					605			
Gln	Glu	Leu	Asn	Asp	Leu	Val	Thr	Ser	Thr	Leu	Asn	Asn	Ser	Ile	Pro

610					615					620					
Phe	Glu	Leu	Ser	Ser	Tyr	Thr	Asn	Asp	Lys	Ile	Leu	Ile	Leu	Tyr	Phe
625					630					635					640
Asn	Lys	Leu	Tyr	Lys	Lys	Ile	Lys	Asp	Asn	Ser	Ile	Leu	Asp	Met	Arg
				645					650					655	
Tyr	Glu	Asn	Asn	Lys	Phe	Ile	Asp	Ile	Ser	Gly	Tyr	Gly	Ser	Asn	Ile
			660					665					670		
Ser	Ile	Asn	Gly	Asp	Val	Tyr	Ile	Tyr	Ser	Thr	Asn	Arg	Asn	Gln	Phe
		675					680					685			
Gly	Ile	Tyr	Ser	Ser	Lys	Pro	Ser	Glu	Val	Asn	Ile	Ala	Gln	Asn	Asn
	690					695					700				
Asp	Ile	Ile	Tyr	Asn	Gly	Arg	Tyr	Gln	Asn	Phe	Ser	Ile	Ser	Phe	Trp
705					710					715					720
Val	Arg	Ile	Pro	Lys	Tyr	Phe	Asn	Lys	Val	Asn	Leu	Asn	Asn	Glu	Tyr
				725					730					735	
Thr	Ile	Ile	Asp	Cys	Ile	Arg	Asn	Asn	Asn	Ser	Gly	Trp	Lys	Ile	Ser
			740					745					750		
Leu	Asn	Tyr	Asn	Lys	Ile	Ile	Trp	Thr	Leu	Gln	Asp	Thr	Ala	Gly	Asn
		755					760					765			
Asn	Gln	Lys	Leu	Val	Phe	Asn	Tyr	Thr	Gln	Met	Ile	Ser	Ile	Ser	Asp
	770					775					780				
Tyr	Ile	Asn	Lys	Trp	Ile	Phe	Val	Thr	Ile	Thr	Asn	Asn	Arg	Leu	Gly
785					790					795					800
Asn	Ser	Arg	Ile	Tyr	Ile	Asn	Gly	Asn	Leu	Ile	Asp	Glu	Lys	Ser	Ile
				805					810					815	
Ser	Asn	Leu	Gly	Asp	Ile	His	Val	Ser	Asp	Asn	Ile	Leu	Phe	Lys	Ile
			820					825					830		
Val	Gly	Cys	Asn	Asp	Thr	Arg	Tyr	Val	Gly	Ile	Arg	Tyr	Phe	Lys	Val
		835					840					845			
Phe	Asp	Thr	Glu	Leu	Gly	Lys	Thr	Glu	Ile	Glu	Thr	Leu	Tyr	Ser	Asp
	850					855					860				
Glu	Pro	Asp	Pro	Ser	Ile	Leu	Lys	Asp	Phe	Trp	Gly	Asn	Tyr	Leu	Leu
865					870					875					880
Tyr	Asn	Lys	Arg	Tyr	Tyr	Leu	Leu	Asn	Leu	Leu	Arg	Thr	Asp	Lys	Ser
				885					890					895	
Ile	Thr	Gln	Asn	Ser	Asn	Phe	Leu	Asn	Ile	Asn	Gln	Gln	Arg	Gly	Val
			900					905					910		
Tyr	Gln	Lys	Pro	Asn	Ile	Phe	Ser	Asn	Thr	Arg	Leu	Tyr	Thr	Gly	Val
		915					920					925			
Glu	Val	Ile	Ile	Arg	Lys	Asn	Gly	Ser	Thr	Asp	Ile	Ser	Asn	Thr	Asp
	930					935					940				
Asn	Phe	Val	Arg	Lys	Asn	Asp	Leu	Ala	Tyr	Ile	Asn	Val	Val	Asp	Arg
945					950					955					960
Asp	Val	Glu	Tyr	Arg	Leu	Tyr	Ala	Asp	Ile	Ser	Ile	Ala	Lys	Pro	Glu

965										970					975				
Lys	Ile	Ile	Lys	Leu	Ile	Arg	Thr	Ser	Asn	Ser	Asn	Asn	Ser	Leu	Gly				
			980					985					990						
Gln	Ile	Ile	Val	Met	Asp	Ser	Ile	Gly	Asn	Asn	Cys	Thr	Met	Asn	Phe				
			995				1000					1005							
Gln	Asn	Asn	Asn	Gly	Gly	Asn	Ile	Gly	Leu	Leu	Gly	Phe	His	Ser	Asn				
	1010					1015					1020								
Asn	Leu	Val	Ala	Ser	Ser	Trp	Tyr	Tyr	Asn	Asn	Ile	Arg	Lys	Asn	Thr				
	1025				1030						1035				1040				
Ser	Ser	Asn	Gly	Cys	Phe	Trp	Ser	Phe	Ile	Ser	Lys	Glu	His	Gly	Trp				
				1045				1050						1055					

Gln Glu Asn

<210> 6  
 <211> 1092  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:construct

<400> 6

Met	Leu	Ser	Arg	Ala	Val	Cys	Gly	Thr	Ser	Arg	Gln	Leu	Ala	Pro	Ala
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Leu	Gly	Tyr	Leu	Gly	Ser	Arg	Gln	Lys	His	Ser	Arg	Gly	Ser	Pro	Ala
			20					25					30		
Leu	Pro	Tyr	Pro	Tyr	Asp	Ala	Leu	Glu	Pro	His	Ile	Asp	Lys	Glu	Thr
		35					40					45			
Met	Asn	Ile	His	His	Thr	Lys	His	His	Asn	Thr	Tyr	Val	Thr	Asn	Leu
	50					55					60				
Asn	Ala	Ala	Leu	Glu	Gly	His	Pro	Asp	Leu	Gln	Asn	Lys	Ser	Leu	Glu
	65				70					75					80
Glu	Leu	Leu	Ser	Asn	Leu	Glu	Ala	Leu	Pro	Glu	Ser	Ile	Arg	Thr	Ala
				85					90					95	
Val	Arg	Asn	Asn	Gly	Gly	Gly	His	Ala	Asn	His	Ser	Leu	Phe	Trp	Thr
			100					105					110		
Ile	Leu	Ser	Pro	Asn	Gly	Gly	Gly	Glu	Pro	Thr	Gly	Glu	Leu	Ala	Asp
		115				120						125			
Ala	Ile	Asn	Lys	Lys	Phe	Gly	Ser	Phe	Thr	Ala	Phe	Lys	Asp	Glu	Phe
	130					135					140				
Ser	Lys	Ala	Ala	Ala	Gly	Arg	Phe	Gly	Ser	Gly	Trp	Ala	Trp	Leu	Val
	145				150					155					160
Val	Asn	Asn	Gly	Glu	Leu	Glu	Ile	Thr	Ser	Thr	Pro	Asn	Gln	Asp	Ser
				165					170					175	
Pro	Ile	Met	Glu	Gly	Lys	Thr	Pro	Ile	Leu	Gly	Leu	Asp	Val	Trp	Glu
			180					185					190		

His	Ala	Tyr	Tyr	Leu	Lys	Tyr	Gln	Asn	Arg	Arg	Pro	Glu	Tyr	Ile	Ala		
		195					200					205					
Ala	Phe	Trp	Asn	Val	Val	Asn	Trp	Asp	Glu	Val	Ala	Lys	Arg	Tyr	Ser		
	210					215					220						
Glu	Ala	Lys	Ala	Lys	Gln	Arg	Ser	Cys	Gly	Leu	Val	Pro	Arg	Gly	Ser		
225					230					235					240		
Gly	Pro	Gly	Ser	Ala	Leu	Asn	Asp	Leu	Cys	Ile	Lys	Val	Asn	Asn	Trp		
				245					250					255			
Asp	Leu	Phe	Phe	Ser	Pro	Ser	Glu	Asp	Asn	Phe	Thr	Asn	Asp	Leu	Asn		
			260					265					270				
Lys	Gly	Glu	Glu	Ile	Thr	Ser	Asp	Thr	Asn	Ile	Glu	Ala	Ala	Glu	Glu		
		275					280					285					
Asn	Ile	Ser	Leu	Asp	Leu	Ile	Gln	Gln	Tyr	Tyr	Leu	Thr	Phe	Asn	Phe		
	290					295					300						
Asp	Asn	Glu	Pro	Glu	Asn	Ile	Ser	Ile	Glu	Asn	Leu	Ser	Ser	Asp	Ile		
305					310					315					320		
Ile	Gly	Gln	Leu	Glu	Leu	Met	Pro	Asn	Ile	Glu	Arg	Phe	Pro	Asn	Gly		
				325					330					335			
Lys	Lys	Tyr	Glu	Leu	Asp	Lys	Tyr	Thr	Met	Phe	His	Tyr	Leu	Arg	Ala		
			340					345					350				
Gln	Glu	Phe	Glu	His	Gly	Lys	Ser	Arg	Ile	Ala	Leu	Thr	Asn	Ser	Val		
		355					360					365					
Asn	Glu	Ala	Leu	Leu	Asn	Pro	Ser	Arg	Val	Tyr	Thr	Phe	Phe	Ser	Ser		
	370				375						380						
Asp	Tyr	Val	Lys	Lys	Val	Asn	Lys	Ala	Thr	Glu	Ala	Ala	Met	Phe	Leu		
385					390					395					400		
Gly	Trp	Val	Glu	Gln	Leu	Val	Tyr	Asp	Phe	Thr	Asp	Glu	Thr	Ser	Glu		
				405					410					415			
Val	Ser	Thr	Thr	Asp	Lys	Ile	Ala	Asp	Ile	Thr	Ile	Ile	Ile	Pro	Tyr		
			420					425					430				
Ile	Gly	Pro	Ala	Leu	Asn	Ile	Gly	Asn	Met	Leu	Tyr	Lys	Asp	Asp	Phe		
		435					440					445					
Val	Gly	Ala	Leu	Ile	Phe	Ser	Gly	Ala	Val	Ile	Leu	Leu	Glu	Phe	Ile		
	450					455					460						
Pro	Glu	Ile	Ala	Ile	Pro	Val	Leu	Gly	Thr	Phe	Ala	Leu	Val	Ser	Tyr		
465					470					475					480		
Ile	Ala	Asn	Lys	Val	Leu	Thr	Val	Gln	Thr	Ile	Asp	Asn	Ala	Leu	Ser		
				485					490					495			
Lys	Arg	Asn	Glu	Lys	Trp	Asp	Glu	Val	Tyr	Lys	Tyr	Ile	Val	Thr	Asn		
			500					505					510				
Trp	Leu	Ala	Lys	Val	Asn	Thr	Gln	Ile	Asp	Leu	Ile	Arg	Lys	Lys	Met		
		515					520					525					
Lys	Glu	Ala	Leu	Glu	Asn	Gln	Ala	Glu	Ala	Thr	Lys	Ala	Ile	Ile	Asn		
	530					535						540					

Tyr Gln Tyr Asn Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe  
545 550 555 560

Asn Ile Asp Asp Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala  
565 570 575

Met Ile Asn Ile Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu  
580 585 590

Met Asn Ser Met Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp  
595 600 605

Ala Ser Leu Lys Asp Ala Leu Leu Lys Tyr Ile Tyr Asp Asn Arg Gly  
610 615 620

Thr Leu Ile Gly Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr  
625 630 635 640

Leu Ser Thr Asp Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln  
645 650 655

Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr  
660 665 670

Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser  
675 680 685

Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro  
690 695 700

Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile  
705 710 715 720

Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn  
725 730 735

Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile  
740 745 750

Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser  
755 760 765

Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln  
770 775 780

Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met  
785 790 795 800

Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr  
805 810 815

Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile  
820 825 830

Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn  
835 840 845

Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp  
850 855 860

Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile  
865 870 875 880

Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe  
885 890 895

Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu  
900 905 910

Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly  
915 920 925

Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile  
930 935 940

Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys  
945 950 955 960

Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val  
965 970 975

Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn  
980 985 990

Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro  
995 1000 1005

Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp  
1010 1015 1020

Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly  
1025 1030 1035 1040

Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys  
1045 1050 1055

Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg  
1060 1065 1070

Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly  
1075 1080 1085

Glu Arg Pro Leu  
1090

<210> 7

<211> 1095

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:construct

<400> 7

Met Leu Ser Arg Ala Val Cys Gly Thr Ser Arg Gln Leu Ala Pro Ala  
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Leu Gly Tyr Leu Gly Ser Arg Gln Lys His Ser Arg Gly Ser Pro Ala  
20 25 30

Leu Pro Tyr Pro Tyr Asp Ala Leu Glu Pro His Ile Asp Lys Glu Thr  
35 40 45

Met Asn Ile His His Thr Lys His His Asn Thr Tyr Val Thr Asn Leu  
50 55 60

Asn Ala Ala Leu Glu Gly His Pro Asp Leu Gln Asn Lys Ser Leu Glu  
65 70 75 80

Glu Leu Leu Ser Asn Leu Glu Ala Leu Pro Glu Ser Ile Arg Thr Ala

85								90						95			
Val	Arg	Asn	Asn	Gly	Gly	Gly	His	Ala	Asn	His	Ser	Leu	Phe	Trp	Thr		
			100					105					110				
Ile	Leu	Ser	Pro	Asn	Gly	Gly	Gly	Glu	Pro	Thr	Gly	Glu	Leu	Ala	Asp		
		115					120					125					
Ala	Ile	Asn	Lys	Lys	Phe	Gly	Ser	Phe	Thr	Ala	Phe	Lys	Asp	Glu	Phe		
		130					135					140					
Ser	Lys	Ala	Ala	Ala	Gly	Arg	Phe	Gly	Ser	Gly	Trp	Ala	Trp	Leu	Val		
145					150					155							
Val	Asn	Asn	Gly	Glu	Leu	Glu	Ile	Thr	Ser	Thr	Pro	Asn	Gln	Asp	Ser		
				165					170					175			
Pro	Ile	Met	Glu	Gly	Lys	Thr	Pro	Ile	Leu	Gly	Leu	Asp	Val	Trp	Glu		
			180					185					190				
His	Ala	Tyr	Tyr	Leu	Lys	Tyr	Gln	Asn	Arg	Arg	Pro	Glu	Tyr	Ile	Ala		
		195					200					205					
Ala	Phe	Trp	Asn	Val	Val	Asn	Trp	Asp	Glu	Val	Ala	Lys	Arg	Tyr	Ser		
		210					215					220					
Glu	Ala	Lys	Ala	Lys	Gln	Arg	Ser	Cys	Gly	Leu	Val	Pro	Arg	Gly	Ser		
225					230					235							
Gly	Pro	Gly	Ser	Lys	Ala	Pro	Gly	Ile	Cys	Ile	Asp	Val	Asp	Asn	Glu		
				245					250					255			
Asp	Leu	Phe	Phe	Ile	Ala	Asp	Lys	Asn	Ser	Phe	Ser	Asp	Asp	Leu	Ser		
			260					265					270				
Lys	Asn	Glu	Arg	Ile	Glu	Tyr	Asn	Thr	Gln	Ser	Asn	Tyr	Ile	Glu	Asn		
		275					280					285					
Asp	Phe	Pro	Ile	Asn	Glu	Leu	Ile	Leu	Asp	Thr	Asp	Leu	Ile	Ser	Lys		
		290					295					300					
Ile	Glu	Leu	Pro	Ser	Glu	Asn	Thr	Glu	Ser	Leu	Thr	Asp	Phe	Asn	Val		
305					310					315							
Asp	Val	Pro	Val	Tyr	Glu	Lys	Gln	Pro	Ala	Ile	Lys	Lys	Ile	Phe	Thr		
			325					330					335				
Asp	Glu	Asn	Thr	Ile	Phe	Gln	Tyr	Leu	Tyr	Ser	Gln	Thr	Phe	Pro	Leu		
			340					345					350				
Asp	Ile	Arg	Asp	Ile	Ser	Leu	Thr	Ser	Ser	Phe	Asp	Asp	Ala	Leu	Leu		
		355					360					365					
Phe	Ser	Asn	Lys	Val	Tyr	Ser	Phe	Phe	Ser	Met	Asp	Tyr	Ile	Lys	Thr		
		370					375					380					
Ala	Asn	Lys	Val	Val	Glu	Ala	Gly	Leu	Phe	Ala	Gly	Trp	Val	Lys	Gln		
385					390					395							
Ile	Val	Asn	Asp	Phe	Val	Ile	Glu	Ala	Asn	Lys	Ser	Asn	Thr	Met	Asp		
				405					410					415			
Lys	Ile	Ala	Asp	Ile	Ser	Leu	Ile	Val	Pro	Tyr	Ile	Gly	Leu	Ala	Leu		
			420					425					430				
Asn	Val	Gly	Asn	Glu	Thr	Ala	Lys	Gly	Asn	Phe	Glu	Asn	Ala	Phe	Glu		



435					440					445					
Ile	Ala	Gly	Ala	Ser	Ile	Leu	Leu	Glu	Phe	Ile	Pro	Glu	Leu	Leu	Ile
450						455					460				
Pro	Val	Val	Gly	Ala	Phe	Leu	Leu	Glu	Ser	Tyr	Ile	Asp	Asn	Lys	Asn
465					470					475					480
Lys	Ile	Ile	Lys	Thr	Ile	Asp	Asn	Ala	Leu	Thr	Lys	Arg	Asn	Glu	Lys
				485					490					495	
Trp	Ser	Asp	Met	Tyr	Gly	Leu	Ile	Val	Ala	Gln	Trp	Leu	Ser	Thr	Val
			500					505					510		
Asn	Thr	Gln	Phe	Tyr	Thr	Ile	Lys	Glu	Gly	Met	Tyr	Lys	Ala	Leu	Asn
		515					520					525			
Tyr	Gln	Ala	Gln	Ala	Leu	Glu	Glu	Ile	Ile	Lys	Tyr	Arg	Tyr	Asn	Ile
	530					535					540				
Tyr	Ser	Glu	Lys	Glu	Lys	Ser	Asn	Ile	Asn	Ile	Asp	Phe	Asn	Asp	Ile
545						550					555				560
Asn	Ser	Lys	Leu	Asn	Glu	Gly	Ile	Asn	Gln	Ala	Ile	Asp	Asn	Ile	Asn
				565					570					575	
Asn	Phe	Ile	Asn	Gly	Cys	Ser	Val	Ser	Tyr	Leu	Met	Lys	Lys	Met	Ile
			580					585						590	
Pro	Leu	Ala	Val	Glu	Lys	Leu	Leu	Asp	Phe	Asp	Asn	Thr	Leu	Lys	Lys
		595				600						605			
Asn	Leu	Leu	Asn	Tyr	Ile	Asp	Glu	Asn	Lys	Leu	Tyr	Leu	Ile	Gly	Ser
	610					615					620				
Ala	Glu	Tyr	Glu	Lys	Ser	Lys	Val	Asn	Lys	Tyr	Leu	Lys	Thr	Ile	Met
625						630					635				640
Pro	Phe	Asp	Leu	Ser	Ile	Tyr	Thr	Asn	Asp	Thr	Ile	Leu	Ile	Glu	Met
				645					650					655	
Phe	Asn	Lys	Tyr	Asn	Ser	Glu	Ile	Leu	Asn	Asn	Ile	Ile	Leu	Asn	Leu
			660					665					670		
Arg	Tyr	Lys	Asp	Asn	Asn	Leu	Ile	Asp	Leu	Ser	Gly	Tyr	Gly	Ala	Lys
		675					680					685			
Val	Glu	Val	Tyr	Asp	Gly	Val	Glu	Leu	Asn	Asp	Lys	Asn	Gln	Phe	Lys
	690					695					700				
Leu	Thr	Ser	Ser	Ala	Asn	Ser	Lys	Ile	Arg	Val	Thr	Gln	Asn	Gln	Asn
705						710					715				720
Ile	Ile	Phe	Asn	Ser	Val	Phe	Leu	Asp	Phe	Ser	Val	Ser	Phe	Trp	Ile
				725					730					735	
Arg	Ile	Pro	Lys	Tyr	Lys	Asn	Asp	Gly	Ile	Gln	Asn	Tyr	Ile	His	Asn
			740					745					750		
Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Lys	Asn	Asn	Ser	Gly	Trp	Lys	Ile
		755					760					765			
Ser	Ile	Arg	Gly	Asn	Arg	Ile	Ile	Trp	Thr	Leu	Ile	Asp	Ile	Asn	Gly
	770					775					780				
Lys	Thr	Lys	Ser	Val	Phe	Phe	Glu	Tyr	Asn	Ile	Arg	Glu	Asp	Ile	Ser

785		790		795		800
Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr Asn Asn Leu Asn						
		805		810		815
Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser Asn Thr Asp Ile						
		820		825		830
Lys Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile Ile Phe Lys Leu						
		835		840		845
Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met Lys Tyr Phe Ser						
		850		855		860
Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu Glu Arg Tyr Lys						
		865		870		875
Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly Asn Pro Leu						
		885		890		895
Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly Asn Lys Asn Ser						
		900		905		910
Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu Ile Leu Thr Arg						
		915		920		925
Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr Arg Asp Leu Tyr						
		930		935		940
Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser Gln Ser Ile						
		945		950		955
Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr Leu Asp Phe Phe						
		965		970		975
Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys Tyr Phe Lys Lys						
		980		985		990
Glu Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp Ser Asp Glu Phe						
		995		1000		1005
Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln Pro Thr Tyr Ser						
		1010		1015		1020
Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr Asp Glu Ile Gly						
		1025		1030		1035
Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile Val Phe Glu Glu						
		1045		1050		1055
Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu Lys Glu Val Lys						
		1060		1065		1070
Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp Gln Phe Ile Pro						
		1075		1080		1085
Lys Asp Glu Gly Trp Thr Glu						
		1090		1095		

<210> 8

<211> 1084

<212> PRT

<213> Artificial Sequence

$\langle 220 \rangle$ 

<223> Description of Artificial Sequence:construct

<400> 8

Met 1	Leu	Ser	Arg	Ala 5	Val	Cys	Gly	Thr	Ser 10	Arg	Gln	Leu	Ala	Pro 15	Ala
Leu	Gly	Tyr	Leu 20	Gly	Ser	Arg	Gln	Lys 25	His	Ser	Arg	Gly	Ser 30	Pro	Ala
Leu	Pro	Tyr 35	Pro	Tyr	Asp	Ala	Leu 40	Glu	Pro	His	Ile	Asp 45	Lys	Glu	Thr
Met	Asn 50	Ile	His	His	Thr	Lys 55	His	His	Asn	Thr	Tyr 60	Val	Thr	Asn	Leu
Asn 65	Ala	Ala	Leu	Glu	Gly 70	His	Pro	Asp	Leu	Gln 75	Asn	Lys	Ser	Leu	Glu 80
Glu	Leu	Leu	Ser	Asn 85	Leu	Glu	Ala	Leu	Pro 90	Glu	Ser	Ile	Arg	Thr 95	Ala
Val	Arg	Asn 100	Asn	Gly	Gly	Gly	His	Ala 105	Asn	His	Ser	Leu	Phe 110	Trp	Thr
Ile	Leu	Ser 115	Pro	Asn	Gly	Gly	Gly 120	Glu	Pro	Thr	Gly	Glu 125	Leu	Ala	Asp
Ala	Ile 130	Asn	Lys	Lys	Phe	Gly 135	Ser	Phe	Thr	Ala	Phe 140	Lys	Asp	Glu	Phe
Ser 145	Lys	Ala	Ala	Ala	Gly 150	Arg	Phe	Gly	Ser	Gly 155	Trp	Ala	Trp	Leu	Val 160
Val	Asn	Asn	Gly	Glu 165	Leu	Glu	Ile	Thr	Ser 170	Thr	Pro	Asn	Gln	Asp 175	Ser
Pro	Ile	Met	Glu 180	Gly	Lys	Thr	Pro	Ile 185	Leu	Gly	Leu	Asp	Val 190	Trp	Glu
His	Ala	Tyr 195	Tyr	Leu	Lys	Tyr	Gln 200	Asn	Arg	Arg	Pro	Glu 205	Tyr	Ile	Ala
Ala	Phe 210	Trp	Asn	Val	Val	Asn 215	Trp	Asp	Glu	Val	Ala 220	Lys	Arg	Tyr	Ser
Glu 225	Ala	Lys	Ala	Lys	Gln 230	Arg	Ser	Cys	Gly	Leu 235	Val	Pro	Arg	Gly	Ser 240
Gly	Pro	Gly	Ser	Lys 245	Ala	Pro	Pro	Arg	Leu 250	Cys	Ile	Arg	Val	Asn 255	Asn
Arg	Glu	Leu 260	Phe	Phe	Val	Ala	Ser	Glu 265	Ser	Ser	Tyr	Asn	Glu 270	Asn	Asp
Ile	Asn	Thr 275	Pro	Lys	Glu	Ile	Asp 280	Asp	Thr	Thr	Asn	Leu 285	Asn	Asn	Asn
Tyr	Arg 290	Asn	Asn	Leu	Asp	Glu 295	Val	Ile	Leu	Asp	Tyr 300	Asn	Ser	Glu	Thr
Ile 305	Pro	Gln	Ile	Ser	Asn 310	Gln	Thr	Leu	Asn	Thr 315	Leu	Val	Gln	Asp	Asp 320
Ser	Tyr	Val	Pro	Arg 325	Tyr	Asp	Ser	Asn	Gly 330	Thr	Ser	Glu	Ile	Glu 335	Glu

His	Asn	Val	Val	Asp	Leu	Asn	Val	Phe	Phe	Tyr	Leu	His	Ala	Gln	Lys	
			340					345					350			
Val	Pro	Glu	Gly	Glu	Thr	Asn	Ile	Ser	Leu	Thr	Ser	Ser	Ile	Asp	Thr	
		355					360					365				
Ala	Leu	Ser	Glu	Glu	Ser	Gln	Val	Tyr	Thr	Phe	Phe	Ser	Ser	Glu	Phe	
	370					375					380					
Ile	Asn	Thr	Ile	Asn	Lys	Pro	Val	His	Ala	Ala	Leu	Phe	Ile	Ser	Trp	
385					390				395						400	
Ile	Asn	Gln	Val	Ile	Arg	Asp	Phe	Thr	Thr	Glu	Ala	Thr	Gln	Lys	Ser	
			405					410						415		
Thr	Phe	Asp	Lys	Ile	Ala	Asp	Ile	Ser	Leu	Val	Val	Pro	Tyr	Val	Gly	
			420					425					430			
Leu	Ala	Leu	Asn	Ile	Gly	Asn	Glu	Val	Gln	Lys	Glu	Asn	Phe	Lys	Glu	
		435					440					445				
Ala	Phe	Glu	Leu	Leu	Gly	Ala	Gly	Ile	Leu	Leu	Glu	Phe	Val	Pro	Glu	
	450					455					460					
Leu	Leu	Ile	Pro	Thr	Ile	Leu	Val	Phe	Thr	Ile	Lys	Ser	Phe	Ile	Gly	
465					470					475					480	
Ser	Ser	Glu	Asn	Lys	Asn	Lys	Ile	Ile	Lys	Ala	Ile	Asn	Asn	Ser	Leu	
				485					490					495		
Met	Glu	Arg	Glu	Thr	Lys	Trp	Lys	Glu	Ile	Tyr	Ser	Trp	Ile	Val	Ser	
			500					505					510			
Asn	Trp	Leu	Thr	Arg	Ile	Asn	Thr	Gln	Phe	Asn	Lys	Arg	Lys	Glu	Gln	
		515					520					525				
Met	Tyr	Gln	Ala	Leu	Gln	Asn	Gln	Val	Asp	Ala	Ile	Lys	Thr	Val	Ile	
	530					535					540					
Glu	Tyr	Lys	Tyr	Asn	Asn	Tyr	Thr	Ser	Asp	Glu	Arg	Asn	Arg	Leu	Glu	
545					550					555					560	
Ser	Glu	Tyr	Asn	Ile	Asn	Asn	Ile	Arg	Glu	Glu	Leu	Asn	Lys	Lys	Val	
				565					570					575		
Ser	Leu	Ala	Met	Glu	Asn	Ile	Glu	Arg	Phe	Ile	Thr	Glu	Ser	Ser	Ile	
			580					585					590			
Phe	Tyr	Leu	Met	Lys	Leu	Ile	Asn	Glu	Ala	Lys	Val	Ser	Lys	Leu	Arg	
		595					600					605				
Glu	Tyr	Asp	Glu	Gly	Val	Lys	Glu	Tyr	Leu	Leu	Asp	Tyr	Ile	Ser	Glu	
	610					615					620					
His	Arg	Ser	Ile	Leu	Gly	Asn	Ser	Val	Gln	Glu	Leu	Asn	Asp	Leu	Val	
625					630					635					640	
Thr	Ser	Thr	Leu	Asn	Asn	Ser	Ile	Pro	Phe	Glu	Leu	Ser	Ser	Tyr	Thr	
				645					650					655		
Asn	Asp	Lys	Ile	Leu	Ile	Leu	Tyr	Phe	Asn	Lys	Leu	Tyr	Lys	Lys	Ile	
			660					665					670			
Lys	Asp	Asn	Ser	Ile	Leu	Asp	Met	Arg	Tyr	Glu	Asn	Asn	Lys	Phe	Ile	
		675					680					685				

Asp	Ile	Ser	Gly	Tyr	Gly	Ser	Asn	Ile	Ser	Ile	Asn	Gly	Asp	Val	Tyr
690						695					700				
Ile	Tyr	Ser	Thr	Asn	Arg	Asn	Gln	Phe	Gly	Ile	Tyr	Ser	Ser	Lys	Pro
705					710					715					720
Ser	Glu	Val	Asn	Ile	Ala	Gln	Asn	Asn	Asp	Ile	Ile	Tyr	Asn	Gly	Arg
				725					730					735	
Tyr	Gln	Asn	Phe	Ser	Ile	Ser	Phe	Trp	Val	Arg	Ile	Pro	Lys	Tyr	Phe
			740					745					750		
Asn	Lys	Val	Asn	Leu	Asn	Asn	Glu	Tyr	Thr	Ile	Ile	Asp	Cys	Ile	Arg
		755					760					765			
Asn	Asn	Asn	Ser	Gly	Trp	Lys	Ile	Ser	Leu	Asn	Tyr	Asn	Lys	Ile	Ile
						775					780				
Trp	Thr	Leu	Gln	Asp	Thr	Ala	Gly	Asn	Asn	Gln	Lys	Leu	Val	Phe	Asn
785					790					795					800
Tyr	Thr	Gln	Met	Ile	Ser	Ile	Ser	Asp	Tyr	Ile	Asn	Lys	Trp	Ile	Phe
				805					810					815	
Val	Thr	Ile	Thr	Asn	Asn	Arg	Leu	Gly	Asn	Ser	Arg	Ile	Tyr	Ile	Asn
			820					825					830		
Gly	Asn	Leu	Ile	Asp	Glu	Lys	Ser	Ile	Ser	Asn	Leu	Gly	Asp	Ile	His
		835					840					845			
Val	Ser	Asp	Asn	Ile	Leu	Phe	Lys	Ile	Val	Gly	Cys	Asn	Asp	Thr	Arg
	850					855					860				
Tyr	Val	Gly	Ile	Arg	Tyr	Phe	Lys	Val	Phe	Asp	Thr	Glu	Leu	Gly	Lys
865					870					875					880
Thr	Glu	Ile	Glu	Thr	Leu	Tyr	Ser	Asp	Glu	Pro	Asp	Pro	Ser	Ile	Leu
				885					890					895	
Lys	Asp	Phe	Trp	Gly	Asn	Tyr	Leu	Leu	Tyr	Asn	Lys	Arg	Tyr	Tyr	Leu
			900					905					910		
Leu	Asn	Leu	Leu	Arg	Thr	Asp	Lys	Ser	Ile	Thr	Gln	Asn	Ser	Asn	Phe
		915					920					925			
Leu	Asn	Ile	Asn	Gln	Gln	Arg	Gly	Val	Tyr	Gln	Lys	Pro	Asn	Ile	Phe
						935					940				
Ser	Asn	Thr	Arg	Leu	Tyr	Thr	Gly	Val	Glu	Val	Ile	Ile	Arg	Lys	Asn
945					950					955					960
Gly	Ser	Thr	Asp	Ile	Ser	Asn	Thr	Asp	Asn	Phe	Val	Arg	Lys	Asn	Asp
				965					970					975	
Leu	Ala	Tyr	Ile	Asn	Val	Val	Asp	Arg	Asp	Val	Glu	Tyr	Arg	Leu	Tyr
			980					985					990		
Ala	Asp	Ile	Ser	Ile	Ala	Lys	Pro	Glu	Lys	Ile	Ile	Lys	Leu	Ile	Arg
		995					1000					1005			
Thr	Ser	Asn	Ser	Asn	Asn	Ser	Leu	Gly	Gln	Ile	Ile	Val	Met	Asp	Ser
	1010					1015						1020			
Ile	Gly	Asn	Asn	Cys	Thr	Met	Asn	Phe	Gln	Asn	Asn	Asn	Gly	Gly	Asn
1025				1030						1035					1040

Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val Ala Ser Ser Trp  
1045 1050 1055

Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser Asn Gly Cys Phe Trp  
1060 1065 1070

Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu Asn  
1075 1080

<210> 9

<211> 229

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polypeptide  
comprising a mitochondrial leader from human MnSOD  
and B. Stearothermophilus SOS

<400> 9

Met Leu Ser Arg Ala Val Cys Gly Thr Ser Arg Gln Leu Ala Pro Ala  
1 5 10 15

Leu Gly Tyr Leu Gly Ser Arg Gln Lys His Ser Arg Gly Ser Pro Ala  
20 25 30

Leu Pro Tyr Pro Tyr Asp Ala Leu Glu Pro His Ile Asp Lys Glu Thr  
35 40 45

Met Asn Ile His His Thr Lys His His Asn Thr Tyr Val Thr Asn Leu  
50 55 60

Asn Ala Ala Leu Glu Gly His Pro Asp Leu Gln Asn Lys Ser Leu Glu  
65 70 75 80

Glu Leu Leu Ser Asn Leu Glu Ala Leu Pro Glu Ser Ile Arg Thr Ala  
85 90 95

Val Arg Asn Asn Gly Gly Gly His Ala Asn His Ser Leu Phe Trp Thr  
100 105 110

Ile Leu Ser Pro Asn Gly Gly Gly Glu Pro Thr Gly Glu Leu Ala Asp  
115 120 125

Ala Ile Asn Lys Lys Phe Gly Ser Phe Thr Ala Phe Lys Asp Glu Phe  
130 135 140

Ser Lys Ala Ala Ala Gly Arg Phe Gly Ser Gly Trp Ala Trp Leu Val  
145 150 155 160

Val Asn Asn Gly Glu Leu Glu Ile Thr Ser Thr Pro Asn Gln Asp Ser  
165 170 175

Pro Ile Met Glu Gly Lys Thr Pro Ile Leu Gly Leu Asp Val Trp Glu  
180 185 190

His Ala Tyr Tyr Leu Lys Tyr Gln Asn Arg Arg Pro Glu Tyr Ile Ala  
195 200 205

Ala Phe Trp Asn Val Val Asn Trp Asp Glu Val Ala Lys Arg Tyr Ser  
210 215 220

Glu Ala Lys Ala Lys  
225

<210> 10  
<211> 24  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: modified human  
mitochondrial leader sequence

<400> 10  
Met Leu Ser Arg Ala Val Ser Gly Thr Ser Arg Gln Leu Ala Pro Ala  
1 5 10 15  
Leu Gly Tyr Leu Gly Ser Arg Gln  
20

<210> 11  
<211> 24  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: modified human  
mitochondrial leader sequence

<400> 11  
Met Leu Ser Arg Ala Val Cys Gly Thr Ser Arg Gln Leu Ala Pro Ala  
1 5 10 15  
Leu Gly Tyr Leu Gly Ser Arg Gln  
20

<210> 12  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: linker peptide

<400> 12  
Cys Gly Leu Val Pro Ala Gly Ser Gly Pro  
1 5 10

<210> 13  
<211> 27  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: modified human  
mitochondrial leader sequence

<400> 13  
Met Leu Ser Arg Ala Val Cys Gly Thr Ser Arg Gln Leu Ala Pro Ala  
1 5 10 15  
Leu Gly Tyr Leu Gly Ser Arg Gln Lys His Ser  
20 25

<210> 14

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: modified human  
mitochondrial leader sequence

<400> 14

Met	Leu	Ser	Arg	Ala	Val	Ser	Gly	Thr	Ser	Arg	Gln	Leu	Ala	Pro	Ala
1				5				10					15		

Leu	Gly	Tyr	Leu	Gly	Ser	Arg	Gln	Lys	His	Ser
			20					25		